VVD-050

SUBCLINICAL PORCINE CIRCOVIRUS TYPE 2 (PCV2) INFECTION: DETERMINATION OF DIFFERENT HERD PROFILES SPLIT ACCORDING TO AN OPTIMAL SEROLOGICAL CRITERION

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Introduction

PCV2 is associated with various disease conditions known as porcine circovirus diseases (PCVD). PCV2 infection dynamics play a role in PCVD. However, few data are available on PCV2 infection dynamics in herds without signs of PCVD. The study aimed at 1/ assessing PCV2 infection dynamics in herds with subclinical PCV2 disease and without PCV2 piglet vaccination and 2/ identifying a serological criterion to discriminate between PCV2 infection profiles.

Material&Methods

The study was carried out in 41 French herds. In each herd, 20 finishers from 2 batches were bled (10/12-week-old pigs and at least 22-week-old pigs). Serum samples were tested by the commercial SERELISA®PCV2 Ab Mono Blocking test to detect PCV2 antibodies. The serological results were used to identify different PCV2 infection profiles by hierarchical clustering (FactoMineR, R software). Then the most contributing variable to the cluster building process was sought by a discriminant analysis (R software). The cut-off allowing the allocation of the herds in different PCV2 infection profiles and minimising the classification errors has been determined by a ROC curve (ROCR, R software).

Results

Two groups of herds were identified. Group 1 comprised 20 herds with low frequencies of pigs with high SERELISA® values and small mean and maximal SERELISA® values in both batches. The second group had higher SERELISA® values on these parameters indicating an early exposure to PCV2 and/or a higher infection pressure or intensity of exposure to PCV2 in this group. Having at least 40% of 22-week-old pigs with a SERELISA® result>5000 was found to be the best criterion to allocate the herds to this second group (sensitivity=100%, specificity=95%).

Discussion&Conclusion

Different PCV2 infection dynamics occurred in herds without PCVD signs. A serological criterion based on the SERELISA® results was defined to gain insight into the diagnostic of PCV2 infection patterns in subclinically infected herds.